

<!--StartFragment-->RESULT 2

OSU95968

LOCUS OSU95968 999 bp mRNA linear PLN 01-MAY-2000
DEFINITION Oryza sativa beta-expansin (EXPB2) mRNA, complete cds.

ACCESSION U95968

VERSION U95968.1 GI:2224914

KEYWORDS

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 999)

AUTHORS Shcherban,T.Y., Shi,J., Durachko,D.M., Guiltinan,M.J.,
McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.

TITLE Molecular cloning and sequence analysis of expansins--a highly
conserved, multigene family of proteins that mediate cell wall
extension in plants

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)
PUBMED 7568110

REFERENCE 2 (bases 1 to 999)

AUTHORS Cosgrove,D.J., Bedinger,P. and Durachko,D.M.

TITLE Group I allergens of grass pollen as cell wall-loosening agents

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6559-6564 (1997)
PUBMED 9177257

REFERENCE 3 (bases 1 to 999)

AUTHORS Cosgrove,D.J.

TITLE Direct Submission

JOURNAL Submitted (01-APR-1997) Biology, Penn State University, 208 Mueller
Lab, University Park, PA 16802, USA

FEATURES

source

Location/Qualifiers

1. .999

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

gene

1. .999

/gene="EXPB2"

CDS

70. .855

/gene="EXPB2"

/note="cell wall loosening protein"

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/protein_id="AAB61710.1"

/db_xref="GI:2224915"

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VIITDMNYYPVARYHFDLSGTAFGAMARPGNDQLRHAGIIDIQFRRVPCYHRGLYVN
FHVEAGSNPVYLAFLVEFANKDGTVVQLDVMESLPSGKPTRVWTPMRRSWGSIWRLDA
NHRLOGPXSLRMVSESGQTVIAHQVIPANWRANTNYGSKVQFR"

ORIGIN

Alignment Scores:

Pred. No.:	8.27e-117	Length:	999
Score:	1415.00	Matches:	261
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	15	Gaps:	0

US-10-730-866-10 (1-261) x OSU95968 (1-999)

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Qy 21 PheAlaAlaGlyValValTyrThrAsnAspTrpLeuProAlaLysAlaThrTrpTyrGly 40
 Db 130 TTCGCCGCCGGCGTCGTCTACACCAACGACTGGCTCCCGGCCAAGGCCACCTGGTACGGC 189

Qy 41 GlnProAsnGlyAlaGlyProAspAspAsnGlyGlyAlaCysGlyPheLysAsnThrAsn 60
 Db 190 CAGCCCAACGGCGCCGGACCCGACACAACGGCGGTGCGTGCGGGTTCAAGAACACCAAC 249

Qy 61 GlnTyrProPheMetSerMetThrSerCysGlyAsnGluProLeuPheGlnAspGlyLys 80
 Db 250 CAGTACCCGTTTCATGTCCATGACCTCCTGCGGCAACGAGCCTCTGTTCCAGGACGGCAAG 309

Qy 81 GlyCysGlyAlaCysTyrGlnIleArgCysThrAsnAsnProSerCysSerGlyGlnPro 100
 Db 310 GGCTGTGGCGCCTGCTACCAGATACGGTGCACCAACAACCCGTCGTGCTCCGGGCGGCGC 369

Qy 101 ArgThrValIleIleThrAspMetAsnTyrTyrProValAlaArgTyrHisPheAspLeu 120
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 Db 490 GGCATCATCGACATCCAGTTCAGGCGCGTCCCGTGCTACCACGCGGCCTCTACGTGAAC 549

Qy 161 PheHisValGluAlaGlySerAsnProValTyrLeuAlaValLeuValGluPheAlaAsn 180
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Qy 181 LysAspGlyThrValValGlnLeuAspValMetGluSerLeuProSerGlyLysProThr 200
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Qy 241 HisGlnValIleProAlaAsnTrpArgAlaAsnThrAsnTyrGlySerLysValGlnPhe 260
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Qy 261 Arg 261
 Db 850 CGT 852
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